

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 3914-3

In re patent application of

IUCHI, SATOSHI et al.

Serial No. 09/758,269

Filed: January 12, 2001



For: TRANSGENIC PLANTS CARRYING NEOXANTHIN CLEAVAGE ENZYME GENE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231

Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

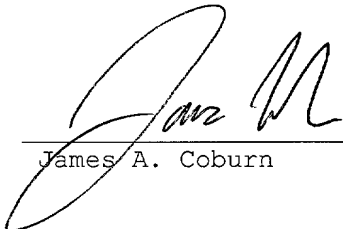
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/758,269

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

June 25, 2001
Date


James A. Coburn

HARBOR CONSULTING
Intellectual Property Services
1500A Lafayette Road
Suite 262
Portsmouth, N.H.
800-318-3021



SEQUENCE LISTING

<110> IUCHI, SATOSHI
KOBAYASHI, MASATOMO
SHINOZAKI, KAZUO

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CLEAVAGE ENZYME GENE

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<141> 2001-01-12

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 Arg Tyr Asp Phe Asp Gly Lys Leu Ala Met Ser Met Thr Ala His Pro
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 Lys Thr Asp Pro Ile Thr Gly Glu Thr Phe Ala Phe Arg Tyr Gly Pro
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 Val Pro Pro Phe Leu Thr Tyr Phe Arg Phe Asp Ser Ala Gly Lys Lys
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 Gln Arg Asp Val Pro Ile Phe Ser Met Thr Ser Pro Ser Phe Leu His
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Gln Ile Val Asn Ala Val Ser Leu Glu Val Glu Ala Thr Val Lys Leu
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Ser Gly Asn Phe Ala Pro Ile Arg Asp Glu Thr Pro Pro Val Lys Asp
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 Pro Thr Lys Lys Ala Arg Phe Gly Val Leu Pro Arg Tyr Ala Lys Asp
 305 310 315 320

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Met Gln His Ser Leu Arg Ser Asp Leu Leu Pro Thr Lys Thr Ser Pro
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cgt tct cat tta ctt cca caa ccc aaa aat gca aat att tct cga cga	96
Arg Ser His Leu Leu Pro Gln Pro Lys Asn Ala Asn Ile Ser Arg Arg	
20 25 30	
att ctc att aac cct ttc aag ata ccg aca ctt cct gat ctc act tct	144
Ile Leu Ile Asn Pro Phe Lys Ile Pro Thr Leu Pro Asp Leu Thr Ser	
35 40 45	
ccg gtt ccg tca ccg gtt aag ctc aaa cca acg tat cca aac tta aac	192
Pro Val Pro Ser Pro Val Lys Leu Lys Pro Thr Tyr Pro Asn Leu Asn	
50 55 60	
ctt ctt cag aag cta gcg gct acg atg ctc gac aag att gag tcc tct	240
Leu Leu Gln Lys Leu Ala Ala Thr Met Leu Asp Lys Ile Glu Ser Ser	
65 70 75 80	
atc gtt att cct atg gag cag aat cgc ccg ctt cct aaa ccg acc gac	288
Ile Val Ile Pro Met Glu Gln Asn Arg Pro Leu Pro Lys Pro Thr Asp	
85 90 95	
ccg gcg gtt caa tta tca ggt aac ttc gct ccg gtt aat gaa tgt ccg	336
Pro Ala Val Gln Leu Ser Gly Asn Phe Ala Pro Val Asn Glu Cys Pro	
100 105 110	
gtt cag aac ggt tta gaa gtg gtt ggt cag att cct tct tgt cta aaa	384
Val Gln Asn Gly Leu Glu Val Val Gly Gln Ile Pro Ser Cys Leu Lys	
115 120 125	
gga gtt tac atc cgt aac ggt gca aac cct atg ttt ccg ccg tta gcc	432
Gly Val Tyr Ile Arg Asn Gly Ala Asn Pro Met Phe Pro Pro Leu Ala	
130 135 140	
gga cat cat tta ttt gac ggt gac gga atg att cac gcc gtt agt atc	480
Gly His His Leu Phe Asp Gly Asp Gly Met Ile His Ala Val Ser Ile	
145 150 155 160	
ggt ttt gat aac cag gtt agt tac agc tgc cgg tac act aaa aca aac	528
Gly Phe Asp Asn Gln Val Ser Tyr Ser Cys Arg Tyr Thr Lys Thr Asn	
165 170 175	
cgg ctt gtt caa gaa acc gcg ctt gga cga tcg gtt ttc cct aaa cca	576
Arg Leu Val Gln Glu Thr Ala Leu Gly Arg Ser Val Phe Pro Lys Pro	
180 185 190	
atc ggc gag ctt cac ggc cat tcc ggt cta gct cga ctc gct ctc ttc	624
Ile Gly Glu Leu His Gly His Ser Gly Leu Ala Arg Leu Ala Leu Phe	
195 200 205	
acg gct cga gct ggg atc ggt cta gtg gac ggg aca cgt ggc atg ggc	672
Thr Ala Arg Ala Gly Ile Gly Leu Val Asp Gly Thr Arg Gly Met Gly	
210 215 220	
gta gct aac gcc ggt gtg gtt ttc ttt aac ggc agg tta tta gcc atg	720
Val Ala Asn Ala Gly Val Val Phe Phe Asn Gly Arg Leu Leu Ala Met	
225 230 235 240	

tca gaa gat gat ctt cct tac caa gtg aag atc gac ggt caa gga gat	768
Ser Glu Asp Asp Leu Pro Tyr Gln Val Lys Ile Asp Gly Gln Gly Asp	
245 250 255	
ctt gag acg atc gga cgg ttc gga ttc gat gac cag att gac tct tca	816
Leu Glu Thr Ile Gly Arg Phe Gly Phe Asp Asp Gln Ile Asp Ser Ser	
260 265 270	
gtg ata gcg cat cct aag gtg gac gcg acc aca gga gat ctc cat aca	864
Val Ile Ala His Pro Lys Val Asp Ala Thr Thr Gly Asp Leu His Thr	
275 280 285	
ctg agc tac aac gtt ttg aag aaa cct cat ctc agg tat ctt aaa ttc	912
Leu Ser Tyr Asn Val Leu Lys Lys Pro His Leu Arg Tyr Leu Lys Phe	
290 295 300	
aac acg tgc ggg aaa aag aca cgt gac gtg gag atc acg ctc cct gaa	960
Asn Thr Cys Gly Lys Lys Thr Arg Asp Val Glu Ile Thr Leu Pro Glu	
305 310 315 320	
cca acg atg att cat gat ttc gcg ata acc gag aat ttt gtc gtt ata	1008
Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn Phe Val Val Ile	
325 330 335	
ccg gat cag caa atg gta ttc aaa tta tcc gaa atg att cgg ggc ggg	1056
Pro Asp Gln Gln Met Val Phe Lys Leu Ser Glu Met Ile Arg Gly Gly	
340 345 350	
tca ccc gtt atc tac gtt aaa gaa aaa atg gcg aga ttt gga gtt ttg	1104
Ser Pro Val Ile Tyr Val Lys Glu Lys Met Ala Arg Phe Gly Val Leu	
355 360 365	
tca aag cag gat ctg acc ggg tcg gat ata aat tgg gtt gat gta ccg	1152
Ser Lys Gln Asp Leu Thr Gly Ser Asp Ile Asn Trp Val Asp Val Pro	
370 375 380	
gat tgt ttc tgt ttc cat cta tgg aat gcg tgg gaa gag aga acc gaa	1200
Asp Cys Phe Cys Phe His Leu Trp Asn Ala Trp Glu Glu Arg Thr Glu	
385 390 395 400	
gag gga gac cca gtt atc gtc gta atc ggg tca tgt atg agc cca ccc	1248
Glu Gly Asp Pro Val Ile Val Val Ile Gly Ser Cys Met Ser Pro Pro	
405 410 415	
gac acg atc ttt agt gaa tca gga gaa cca acc cgg gtt gaa tta agt	1296
Asp Thr Ile Phe Ser Glu Ser Gly Glu Pro Thr Arg Val Glu Leu Ser	
420 425 430	
gag atc cgg tta aac atg cgt aca aaa gaa tcg aac cgt aag gtt atc	1344
Glu Ile Arg Leu Asn Met Arg Thr Lys Glu Ser Asn Arg Lys Val Ile	
435 440 445	
gta acc gga gtg aat tta gaa gcg ggt cac ata aac cgt agt tac gtg	1392
Val Thr Gly Val Asn Leu Glu Ala Gly His Ile Asn Arg Ser Tyr Val	
450 455 460	

ggc cgg aaa agc cag ttc gtt tac ata gca ata gcc gat cct tgg ccc 1440
 Gly Arg Lys Ser Gln Phe Val Tyr Ile Ala Ile Ala Asp Pro Trp Pro
 465 470 475 480

aaa tgc agt ggc att gcg aag gta gat ata caa aac ggc acc gtt tca 1488
 Lys Cys Ser Gly Ile Ala Lys Val Asp Ile Gln Asn Gly Thr Val Ser
 485 490 495

gag ttt aat tac gga ccg agc cgg ttc ggt gga gaa ccg tgc ttt gta 1536
 Glu Phe Asn Tyr Gly Pro Ser Arg Phe Gly Gly Glu Pro Cys Phe Val
 500 505 510

ccg gag gga gaa gga gaa gaa gac aaa ggt tat gta atg ggg ttt gtg 1584
 Pro Glu Gly Glu Gly Glu Glu Asp Lys Gly Tyr Val Met Gly Phe Val
 515 520 525

aga gac gaa gag aaa gac gag tcg gag ttt gtg gtg gtc gac gcg acg 1632
 Arg Asp Glu Glu Lys Asp Glu Ser Glu Phe Val Val Val Asp Ala Thr
 530 535 540

gat atg aag caa gtc gcg gcg gtg cgc ttg ccg gag agg gta cct tat 1680
 Asp Met Lys Gln Val Ala Ala Val Arg Leu Pro Glu Arg Val Pro Tyr
 545 550 555 560

ggt ttc cat gga acg ttc gtg agc gag aat cag ttg aag gaa caa gtt 1728
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 565 570 575

ttc tga 1734
 Phe

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<211> 577

<212> PRT

<213> Arabidopsis thaliana

<400> 10

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Arg Ser His Leu Leu Pro Gln Pro Lys Asn Ala Asn Ile Ser Arg Arg
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Ile Leu Ile Asn Pro Phe Lys Ile Pro Thr Leu Pro Asp Leu Thr Ser
 35 40 45

Pro Val Pro Ser Pro Val Lys Leu Lys Pro Thr Tyr Pro Asn Leu Asn
 50 55 60

Leu Leu Gln Lys Leu Ala Ala Thr Met Leu Asp Lys Ile Glu Ser Ser
 65 70 75 80

Ile Val Ile Pro Met Glu Gln Asn Arg Pro Leu Pro Lys Pro Thr Asp
 85 90 95

Pro Ala Val Gln Leu Ser Gly Asn Phe Ala Pro Val Asn Glu Cys Pro
 100 105 110

Val Gln Asn Gly Leu Glu Val Val Gly Gln Ile Pro Ser Cys Leu Lys
 115 120 125
 Gly Val Tyr Ile Arg Asn Gly Ala Asn Pro Met Phe Pro Pro Leu Ala
 130 135 140
 Gly His His Leu Phe Asp Gly Asp Gly Met Ile His Ala Val Ser Ile
 145 150 155 160
 Gly Phe Asp Asn Gln Val Ser Tyr Ser Cys Arg Tyr Thr Lys Thr Asn
 165 170 175
 Arg Leu Val Gln Glu Thr Ala Leu Gly Arg Ser Val Phe Pro Lys Pro
 180 185 190
 Ile Gly Glu Leu His Gly His Ser Gly Leu Ala Arg Leu Ala Leu Phe
 195 200 205
 Thr Ala Arg Ala Gly Ile Gly Leu Val Asp Gly Thr Arg Gly Met Gly
 210 215 220
 Val Ala Asn Ala Gly Val Val Phe Phe Asn Gly Arg Leu Leu Ala Met
 225 230 235 240
 Ser Glu Asp Asp Leu Pro Tyr Gln Val Lys Ile Asp Gly Gln Gly Asp
 245 250 255
 Leu Glu Thr Ile Gly Arg Phe Gly Phe Asp Asp Gln Ile Asp Ser Ser
 260 265 270
 Val Ile Ala His Pro Lys Val Asp Ala Thr Thr Gly Asp Leu His Thr
 275 280 285
 Leu Ser Tyr Asn Val Leu Lys Lys Pro His Leu Arg Tyr Leu Lys Phe
 290 295 300
 Asn Thr Cys Gly Lys Lys Thr Arg Asp Val Glu Ile Thr Leu Pro Glu
 305 310 315 320
 Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn Phe Val Val Ile
 325 330 335
 Pro Asp Gln Gln Met Val Phe Lys Leu Ser Glu Met Ile Arg Gly Gly
 340 345 350
 Ser Pro Val Ile Tyr Val Lys Glu Lys Met Ala Arg Phe Gly Val Leu
 355 360 365
 Ser Lys Gln Asp Leu Thr Gly Ser Asp Ile Asn Trp Val Asp Val Pro
 370 375 380
 Asp Cys Phe Cys Phe His Leu Trp Asn Ala Trp Glu Glu Arg Thr Glu
 385 390 395 400
 Glu Gly Asp Pro Val Ile Val Val Ile Gly Ser Cys Met Ser Pro Pro
 405 410 415

Asp Thr Ile Phe Ser Glu Ser Gly Glu Pro Thr Arg Val Glu Leu Ser
 420 425 430

Glu Ile Arg Leu Asn Met Arg Thr Lys Glu Ser Asn Arg Lys Val Ile
 435 440 445

Val Thr Gly Val Asn Leu Glu Ala Gly His Ile Asn Arg Ser Tyr Val
 450 455 460

Gly Arg Lys Ser Gln Phe Val Tyr Ile Ala Ile Ala Asp Pro Trp Pro
 465 470 475 480

Lys Cys Ser Gly Ile Ala Lys Val Asp Ile Gln Asn Gly Thr Val Ser
 485 490 495

Glu Phe Asn Tyr Gly Pro Ser Arg Phe Gly Gly Glu Pro Cys Phe Val
 500 505 510

Pro Glu Gly Glu Gly Glu Glu Asp Lys Gly Tyr Val Met Gly Phe Val
 515 520 525

Arg Asp Glu Glu Lys Asp Glu Ser Glu Phe Val Val Val Asp Ala Thr
 530 535 540

Asp Met Lys Gln Val Ala Ala Val Arg Leu Pro Glu Arg Val Pro Tyr
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Gly Phe His Gly Thr Phe Val Ser Glu Asn Gln Leu Lys Glu Gln Val
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Phe

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<211> 1839

<212> DNA

<213> Vigna unguiculata

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<221> CDS

<222> (1)..(1836)

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ccc ccc ttc aaa gac cta cct tcc aca tct tct ccc aca aac tta ctt 96
 Pro Pro Phe Lys Asp Leu Pro Ser Thr Ser Ser Pro Thr Asn Leu Leu
 20 25 30

cct tta agg aaa aca tcc tct tcc aac acc atc aca tgt tcc ctt caa 144
 Pro Leu Arg Lys Thr Ser Ser Ser Asn Thr Ile Thr Cys Ser Leu Gln
 35 40 45

aca ctc cac ttc ccc aaa cag tac caa cca aca tcc aca tcc aca tcc 192
 Thr Leu His Phe Pro Lys Gln Tyr Gln Pro Thr Ser Thr Ser Thr Ser
 50 55 60

aca gcc acc acc aca aca ccc acc cca atc aaa act acc acc atc acc	240
Thr Ala Thr Thr Thr Thr Pro Thr Pro Ile Lys Thr Thr Thr Ile Thr	
65 70 75 80	
acc acc aca ccg ccc agg gaa acc aac cct ctc tct gac acc aac caa	288
Thr Thr Thr Pro Pro Arg Glu Thr Asn Pro Leu Ser Asp Thr Asn Gln	
85 90 95	
cca tta cct caa aaa tgg aac ttt ctc cag aaa gcc gct gcc acg gcc	336
Pro Leu Pro Gln Lys Trp Asn Phe Leu Gln Lys Ala Ala Ala Thr Ala	
100 105 110	
ttg gac ctg gtc gaa acg gcg ctc gtc tcg cac gag cgc aaa cac ccg	384
Leu Asp Leu Val Glu Thr Ala Leu Val Ser His Glu Arg Lys His Pro	
115 120 125	
ctc ccc aaa acg gcg gac ccg agg gtc caa atc gcc ggg aac ttc gcg	432
Leu Pro Lys Thr Ala Asp Pro Arg Val Gln Ile Ala Gly Asn Phe Ala	
130 135 140	
ccg gtg ccg gag cat gcc gcg gat caa gga ctc ccg gtg gtc gga aaa	480
Pro Val Pro Glu His Ala Ala Asp Gln Gly Leu Pro Val Val Gly Lys	
145 150 155 160	
atc ccc aaa tgc att gac ggc gtg tac gtg cgc aac ggt gcc aat ccg	528
Ile Pro Lys Cys Ile Asp Gly Val Tyr Val Arg Asn Gly Ala Asn Pro	
165 170 175	
ctc tac gag cct gtg gcc ggg cac cac ttc ttc gac ggc gac ggc atg	576
Leu Tyr Glu Pro Val Ala Gly His His Phe Phe Asp Gly Asp Gly Met	
180 185 190	
gtc cac gcc gtg aag ttc acg aac ggc gcc gcc agc tac gcc tgc cgc	624
Val His Ala Val Lys Phe Thr Asn Gly Ala Ala Ser Tyr Ala Cys Arg	
195 200 205	
ttc acc gag acg cag cgt ctc tcg cag gag aaa tct cta ggc cgc ccg	672
Phe Thr Glu Thr Gln Arg Leu Ser Gln Glu Lys Ser Leu Gly Arg Pro	
210 215 220	
gtg ttc ccg aag gcc atc ggg gag ctc cac ggc cac tcc ggc atc gcg	720
Val Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Ser Gly Ile Ala	
225 230 235 240	
cgg ctc ctc ctc ttc tac gcg cgc ggt ctc ttc ggg ctc gtt gat ggg	768
Arg Leu Leu Leu Phe Tyr Ala Arg Gly Leu Phe Gly Leu Val Asp Gly	
245 250 255	
tcc cag ggc atg ggc gtg gcg aac gcc ggt ctc gtc tac ttc aac aac	816
Ser Gln Gly Met Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn Asn	
260 265 270	
cac ctc ttg gcc atg tcc gaa gac gat tta ccc tac cac gtg aga atc	864
His Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr His Val Arg Ile	
275 280 285	

acc Thr	cct Pro	aac Asn	ggc Gly	gac Asp	tta Leu	acc Thr	acc Thr	gtt Val	ggc Gly	cgt Arg	tac Tyr	gac Asp	ttc Phe	aac Asn	ggg Gly	912	
290						295			300								
cag Gln	ctc Leu	aac Asn	tca Ser	aca Thr	atg Met	atc Ile	gcc Ala	cac His	ccg Pro	aaa Lys	ctg Leu	gac Asp	ccc Pro	gtc Val	gac Asp	960	
305			310						315			320					
ggc Gly	gac Asp	ctc Leu	cac His	gcg Ala	ctc Leu	agc Ser	tac Tyr	gac Asp	gtc Val	att Ile	cag Gln	aag Lys	cct Pro	tac Tyr	ctc Leu	1008	
			325						330			335					
aag Lys	tac Tyr	ttc Phe	cgt Arg	ttc Phe	tcc Ser	ccc Pro	gac Asp	ggc Gly	gtc Val	aag Lys	tcc Ser	ccc Pro	gac Asp	gtg Val	gaa Glu	1056	
			340						345			350					
atc Ile	ccc Pro	ctg Leu	aag Lys	gag Glu	ccc Pro	acc Thr	atg Met	atg Met	cac His	gat Asp	ttc Phe	gcc Ala	ata Ile	acg Thr	gag Glu	1104	
			355			360						365					
aat Asn	ttc Phe	gtc Val	gtc Val	gtc Val	ccc Pro	gac Asp	cag Gln	cag Gln	gtg Val	gtc Val	ttc Phe	aaa Lys	cta Leu	acg Thr	gag Glu	1152	
370						375						380					
atg Met	atc Ile	acc Thr	ggc Gly	ggg Gly	tcc Ser	ccc Pro	gtg Val	gtc Val	tac Tyr	gac Asp	aag Lys	aac Asn	aaa Lys	acc Thr	tca Ser	1200	
385						390						395			400		
cgg Arg	ttt Phe	ggg Gly	att Ile	ctg Leu	cac His	aag Lys	aat Asn	gcg Ala	aag Lys	gac Asp	gcg Ala	aat Asn	gcg Ala	atg Met	cgg Arg	1248	
			405						410			415					
tgg Trp	atc Ile	gac Asp	gcg Ala	ccg Pro	gat Asp	tgt Cys	ttc Phe	tgc Cys	ttc Phe	cac His	ctc Leu	tgg Trp	aac Asn	gcg Ala	tgg Trp	1296	
			420						425			430					
gag Glu	gag Glu	ccc Pro	gaa Glu	acc Thr	gag Glu	gag Glu	gtt Val	gtg Val	gtg Val	att Ile	ggg Gly	tcc Ser	tgc Cys	atg Met	acc Thr	1344	
435						440						445					
cct Pro	gcg Ala	gac Asp	tcc Ser	att Ile	ttc Phe	aac Asn	gaa Glu	tgc Cys	gag Glu	gag Glu	agt Ser	ttg Leu	aag Lys	agc Ser	gtg Val	1392	
450						455						460					
ctg Leu	tca Ser	gag Glu	ata Ile	agg Arg	ctg Leu	aac Asn	ttg Leu	agg Arg	acc Thr	ggc Gly	aag Lys	tcc Ser	act Thr	cgg Arg	cgc Arg	1440	
465						470						475			480		
ccc Pro	att Ile	atc Ile	tcc Ser	gac Asp	gcc Ala	gaa Glu	caa Gln	gtg Val	aac Asn	ctg Leu	gaa Glu	gcc Ala	ggc Gly	atg Met	gtg Val	1488	
			485						490			495					
aac Asn	aga Arg	aac Asn	aag Lys	ctc Leu	gga Gly	agg Arg	aag Lys	acc Thr	cag Gln	ttc Phe	gcg Ala	tat Tyr	ctg Leu	gct Ala	ctg Leu	1536	
			500						505			510					

gcg gag ccc tgg ccc aaa gtc tcg ggc ttt gcg aaa gtt gat ttg ctg 1584
 Ala Glu Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu Leu
 515 520 525

agt ggg gaa gtg aag aag tac atg tat gga gaa gag aag ttc ggt ggg 1632
 Ser Gly Glu Val Lys Lys Tyr Met Tyr Gly Glu Glu Lys Phe Gly Gly
 530 535 540

gag cct ctg ttt ctt ccc aac ggc caa aaa gaa gac gat ggg tat att 1680
 Glu Pro Leu Phe Leu Pro Asn Gly Gln Lys Glu Asp Asp Gly Tyr Ile
 545 550 555 560

ctg gca ttc gtg cac gac gag aaa gaa tgg aaa tcc gag ctg cag att 1728
 Leu Ala Phe Val His Asp Glu Lys Glu Trp Lys Ser Glu Leu Gln Ile
 565 570 575

gtg aat gcc caa aat tta aag ctc gaa gct tcc atc aaa ctc ccc tct 1776
 Val Asn Ala Gln Asn Leu Lys Leu Glu Ala Ser Ile Lys Leu Pro Ser
 580 585 590

cgt gtt ccc tac ggt ttt cat gga act ttc att cat tcc aag gat ttg 1824
 Arg Val Pro Tyr Gly Phe His Gly Thr Phe Ile His Ser Lys Asp Leu
 595 600 605

agg aaa caa gct tga
 Arg Lys Gln Ala 1839
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<210> 12

<211> 612

<212> PRT

<213> Vigna unguiculata

<400> 12

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Pro Leu Arg Lys Thr Ser Ser Ser Asn Thr Ile Thr Cys Ser Leu Gln
 35 40 45

Thr Leu His Phe Pro Lys Gln Tyr Gln Pro Thr Ser Thr Ser Thr Ser
 50 55 60

Thr Ala Thr Thr Thr Thr Pro Thr Pro Ile Lys Thr Thr Thr Ile Thr
 65 70 75 80

Thr Thr Thr Pro Pro Arg Glu Thr Asn Pro Leu Ser Asp Thr Asn Gln
 85 90 95

Pro Leu Pro Gln Lys Trp Asn Phe Leu Gln Lys Ala Ala Ala Thr Ala
 100 105 110

Leu Asp Leu Val Glu Thr Ala Leu Val Ser His Glu Arg Lys His Pro
 115 120 125

TCAGAG-6936260

Leu Pro Lys Thr Ala Asp Pro Arg Val Gln Ile Ala Gly Asn Phe Ala
 130 135 140
 Pro Val Pro Glu His Ala Ala Asp Gln Gly Leu Pro Val Val Gly Lys
 145 150 155 160
 Ile Pro Lys Cys Ile Asp Gly Val Tyr Val Arg Asn Gly Ala Asn Pro
 165 170 175
 Leu Tyr Glu Pro Val Ala Gly His His Phe Phe Asp Gly Asp Gly Met
 180 185 190
 Val His Ala Val Lys Phe Thr Asn Gly Ala Ala Ser Tyr Ala Cys Arg
 195 200 205
 Phe Thr Glu Thr Gln Arg Leu Ser Gln Glu Lys Ser Leu Gly Arg Pro
 210 215 220
 Val Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Ser Gly Ile Ala
 225 230 235 240
 Arg Leu Leu Leu Phe Tyr Ala Arg Gly Leu Phe Gly Leu Val Asp Gly
 245 250 255
 Ser Gln Gly Met Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn Asn
 260 265 270
 His Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr His Val Arg Ile
 275 280 285
 Thr Pro Asn Gly Asp Leu Thr Thr Val Gly Arg Tyr Asp Phe Asn Gly
 290 295 300
 Gln Leu Asn Ser Thr Met Ile Ala His Pro Lys Leu Asp Pro Val Asp
 305 310 315 320
 Gly Asp Leu His Ala Leu Ser Tyr Asp Val Ile Gln Lys Pro Tyr Leu
 325 330 335
 Lys Tyr Phe Arg Phe Ser Pro Asp Gly Val Lys Ser Pro Asp Val Glu
 340 345 350
 Ile Pro Leu Lys Glu Pro Thr Met Met His Asp Phe Ala Ile Thr Glu
 355 360 365
 Asn Phe Val Val Val Pro Asp Gln Gln Val Val Phe Lys Leu Thr Glu
 370 375 380
 Met Ile Thr Gly Gly Ser Pro Val Val Tyr Asp Lys Asn Lys Thr Ser
 385 390 395 400
 Arg Phe Gly Ile Leu His Lys Asn Ala Lys Asp Ala Asn Ala Met Arg
 405 410 415
 Trp Ile Asp Ala Pro Asp Cys Phe Cys Phe His Leu Trp Asn Ala Trp
 420 425 430

130 135 140
 145 150 155 160
 165 170 175
 180 185 190
 195 200 205
 210 215 220
 225 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315 320
 325 330 335
 340 345 350
 355 360 365
 370 375 380
 385 390 395 400
 405 410 415
 420 425 430

Glu Glu Pro Glu Thr Glu Glu Val Val Val Ile Gly Ser Cys Met Thr
435 440 445

Pro Ala Asp Ser Ile Phe Asn Glu Cys Glu Glu Ser Leu Lys Ser Val
450 455 460

Leu Ser Glu Ile Arg Leu Asn Leu Arg Thr Gly Lys Ser Thr Arg Arg
465 470 475 480

Pro Ile Ile Ser Asp Ala Glu Gln Val Asn Leu Glu Ala Gly Met Val
485 490 495

Asn Arg Asn Lys Leu Gly Arg Lys Thr Gln Phe Ala Tyr Leu Ala Leu
500 505 510

Ala Glu Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu Leu
515 520 525

Ser Gly Glu Val Lys Lys Tyr Met Tyr Gly Glu Glu Lys Phe Gly Gly
530 535 540

Glu Pro Leu Phe Leu Pro Asn Gly Gln Lys Glu Asp Asp Gly Tyr Ile
545 550 555 560

Leu Ala Phe Val His Asp Glu Lys Glu Trp Lys Ser Glu Leu Gln Ile
565 570 575

Val Asn Ala Gln Asn Leu Lys Leu Glu Ala Ser Ile Lys Leu Pro Ser
580 585 590

Arg Val Pro Tyr Gly Phe His Gly Thr Phe Ile His Ser Lys Asp Leu
595 600 605

Arg Lys Gln Ala
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<210> 13

<211> 1815

<212> DNA

<213> Zea mays

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<221> CDS

<222> (1)..(1812)

<400> 13

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ccg gcc cgg tcc agg gcc cgg gcc tcc aat tcc gtc agg ttc tcg ccg 96
Pro Ala Arg Ser Arg Ala Arg Ala Ser Asn Ser Val Arg Phe Ser Pro
20 25 30

cgc gcc gtc agc tcc gtg ccg ccc gcc gag tgc ctc cag gcg ccg ttc 144
Arg Ala Val Ser Ser Val Pro Pro Ala Glu Cys Leu Gln Ala Pro Phe
35 40 45

cac His	aag Lys 50	ccc Pro	gtc Val	gcc Ala	gac Asp	ctg Leu 55	cct Pro	gcg Ala	ccg Pro	tcc Ser	agg Arg 60	aag Lys	ccc Pro	gcc Ala	gcc Ala	192
att Ile 65	gcc Ala	gtc Val	cca Pro	ggg Gly	cac His 70	gcc Ala	gcg Ala	gcg Ala	ccg Pro	agg Arg 75	aaa Lys	gcg Ala	gag Glu	ggc Gly	ggc Gly 80	240
aag Lys	aag Lys	cag Gln	ctc Leu	aac Asn 85	ttg Leu	ttc Phe	cag Gln	cgc Arg	gcc Ala 90	gcg Ala	gcg Ala	gcc Ala	gcg Ala	ctc Leu 95	gac Asp	288
gcg Ala	ttc Phe	gag Glu	gaa Glu 100	ggg Gly	ttc Phe	gtg Val	gcc Ala	aac Asn 105	gtc Val	ctc Leu	gag Glu	cgg Arg	ccc Pro 110	cac His	ggg Gly	336
ctg Leu	ccc Pro	agc Ser 115	acg Thr	gcc Ala	gac Asp	ccg Pro 120	gcc Ala	gtg Val	cag Gln	atc Ile	gcc Ala 125	ggc Gly	aac Asn	ttc Phe	gcg Ala	384
ccc Pro	gtc Val 130	ggg Gly	gag Glu	agg Arg	ccg Pro	ccc Pro 135	gtg Val	cac His	gag Glu	ctc Leu	ccc Pro 140	gtc Val	tcc Ser	ggc Gly	cgc Arg	432
atc Ile 145	ccg Pro	ccc Pro	ttc Phe	atc Ile	gac Asp 150	ggg Gly	gtc Val	tac Tyr	gcg Ala	cgc Arg 155	aac Asn	ggc Gly	gcc Ala	aac Asn	ccc Pro 160	480
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gtg Val	cac His	gcg Ala	ctg Leu 180	cgg Arg	ata Ile	cgc Arg	aac Asn	ggc Gly 185	gcc Ala	gcc Ala	gag Glu	tcc Ser 190	tac Tyr	gcc Ala	tgc Cys	576
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gcg Ala 225	cgc Arg	ctc Leu	gcc Ala	ctg Leu 230	ttc Phe	tac Tyr	gcg Ala	cgc Arg	gcc Ala	gcg Ala 235	tgc Cys	ggc Gly	ctc Leu	gtg Val	gac Asp 240	720
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ggc Gly	cgc Arg	ctg Leu	ctc Leu 260	gcc Ala	atg Met	tcc Ser	gag Glu	gac Asp 265	gac Asp	ctc Leu	ccc Pro	tac Tyr	cac His	gtc Val	cgc Arg	816

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 Ile Pro Pro Phe Ile Asp Gly Val Tyr Ala Arg Asn Gly Ala Asn Pro
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 Cys Phe Asp Pro Val Ala Gly His His Leu Phe Asp Gly Asp Gly Met
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 Val His Ala Leu Arg Ile Arg Asn Gly Ala Ala Glu Ser Tyr Ala Cys
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Tyr Gln Thr Pro Lys Asn Asn Thr Ile Ser His Pro Lys Gln Glu Asn	
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Ser Gly Asn Phe Ala Pro Val Pro Glu Asn Pro Val Cys Gln Ser Leu	
130 135 140	
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Asn Gly Ala Asn Pro Leu Phe Glu Pro Thr Ala Gly His His Phe Phe	
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Asp Gly Asp Gly Met Val His Ala Val Gln Phe Lys Asn Gly Ser Ala	
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Gln	Lys	Pro	Tyr	Leu	Lys	Tyr	Phe	Arg	Phe	Ser	Lys	Asn	Gly	Glu	Lys
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Arg	Pro	Ser	Lys	Gly	Phe	Ser	Ser	Lys	Leu	Leu	Asp	Leu	Leu	Glu	Arg	
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Leu	Val	Val	Lys	Leu	Met	His	Asp	Ala	Ser	Leu	Pro	Leu	His	Tyr	Leu	
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Tyr Val Ile Lys Val Leu Glu Asp Gly Asp Leu Gln Thr Leu Gly Ile	
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Lys Leu Glu Asn Phe Gly Asn Glu Leu Tyr Glu Met Arg Phe Asn Met	
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Ser Glu Ala Ile Tyr Val Pro Arg Glu Thr Ala Glu Glu Asp Asp Gly	
465 470 475 480	
tac ttg ata ttc ttt gtt cat gat gaa aac aca ggg aaa tca tgc gtg	1488
Tyr Leu Ile Phe Phe Val His Asp Glu Asn Thr Gly Lys Ser Cys Val	
485 490 495	

act gtg ata gac gca aaa aca atg tcg gct gaa ccg gtg gca gtg gtg 1536
 Thr Val Ile Asp Ala Lys Thr Met Ser Ala Glu Pro Val Ala Val Val
 500 505 510

gag ctg ccg cac agg gtc cca tat ggc ttc cat gcc ttg ttt gtt aca 1584
 Glu Leu Pro His Arg Val Pro Tyr Gly Phe His Ala Leu Phe Val Thr
 515 520 525

gag gaa caa ctc cag gaa caa act ctt ata taa 1617
 Glu Glu Gln Leu Gln Glu Gln Thr Leu Ile
 530 535

<210> 18

<211> 538

<212> PRT

<213> Arabidopsis thaliana

<400> 18

Met Ala Glu Lys Leu Ser Asp Gly Ser Ile Ile Ile Ser Val His Pro
 1 5 10 15

Arg Pro Ser Lys Gly Phe Ser Ser Lys Leu Leu Asp Leu Leu Glu Arg
 20 25 30

Leu Val Val Lys Leu Met His Asp Ala Ser Leu Pro Leu His Tyr Leu
 35 40 45

Ser Gly Asn Phe Ala Pro Ile Arg Asp Glu Thr Pro Pro Val Lys Asp
 50 55 60

Leu Pro Val His Gly Phe Leu Pro Glu Cys Leu Asn Gly Glu Phe Val
 65 70 75 80

Arg Val Gly Pro Asn Pro Lys Phe Asp Ala Val Ala Gly Tyr His Trp
 85 90 95

Phe Asp Gly Asp Gly Met Ile His Gly Val Arg Ile Lys Asp Gly Lys
 100 105 110

Ala Thr Tyr Val Ser Arg Tyr Val Lys Thr Ser Arg Leu Lys Gln Glu
 115 120 125

Glu Phe Phe Gly Ala Ala Lys Phe Met Lys Ile Gly Asp Leu Lys Gly
 130 135 140

Phe Phe Gly Leu Leu Met Val Asn Ile Gln Gln Leu Arg Thr Lys Leu
 145 150 155 160

Lys Ile Leu Asp Asn Thr Tyr Gly Asn Gly Thr Ala Asn Thr Ala Leu
 165 170 175

Val Tyr His His Gly Lys Leu Leu Ala Leu Gln Glu Ala Asp Lys Pro
 180 185 190

Tyr Val Ile Lys Val Leu Glu Asp Gly Asp Leu Gln Thr Leu Gly Ile
 195 200 205

Ile Asp Tyr Asp Lys Arg Leu Thr His Ser Phe Thr Ala His Pro Lys
 210 215 220
 Val Asp Pro Val Thr Gly Glu Met Phe Thr Phe Gly Tyr Ser His Thr
 225 230 235 240
 Pro Pro Tyr Leu Thr Tyr Arg Val Ile Ser Lys Asp Gly Ile Met His
 245 250 255
 Asp Pro Val Pro Ile Thr Ile Ser Glu Pro Ile Met Met His Asp Phe
 260 265 270
 Ala Ile Thr Glu Thr Tyr Ala Ile Phe Met Asp Leu Pro Met His Phe
 275 280 285
 Arg Pro Lys Glu Met Val Lys Glu Lys Lys Met Ile Tyr Ser Phe Asp
 290 295 300
 Pro Thr Lys Lys Ala Arg Phe Gly Val Leu Pro Arg Tyr Ala Lys Asp
 305 310 315 320
 Glu Leu Met Ile Arg Trp Phe Glu Leu Pro Asn Cys Phe Ile Phe His
 325 330 335
 Asn Ala Asn Ala Trp Glu Glu Glu Asp Glu Val Val Leu Ile Thr Cys
 340 345 350
 Arg Leu Glu Asn Pro Asp Leu Asp Met Val Ser Gly Lys Val Lys Glu
 355 360 365
 Lys Leu Glu Asn Phe Gly Asn Glu Leu Tyr Glu Met Arg Phe Asn Met
 370 375 380
 Lys Thr Gly Ser Ala Ser Gln Lys Lys Leu Ser Ala Ser Ala Val Asp
 385 390 395 400
 Phe Pro Arg Ile Asn Glu Cys Tyr Thr Gly Lys Lys Gln Arg Tyr Val
 405 410 415
 Tyr Gly Thr Ile Leu Asp Ser Ile Ala Lys Val Thr Gly Ile Ile Lys
 420 425 430
 Phe Asp Leu His Ala Glu Ala Glu Thr Gly Lys Arg Met Leu Glu Val
 435 440 445
 Gly Gly Asn Ile Lys Gly Ile Tyr Asp Leu Gly Glu Gly Arg Tyr Gly
 450 455 460
 Ser Glu Ala Ile Tyr Val Pro Arg Glu Thr Ala Glu Glu Asp Asp Gly
 465 470 475 480
 Tyr Leu Ile Phe Phe Val His Asp Glu Asn Thr Gly Lys Ser Cys Val
 485 490 495
 Thr Val Ile Asp Ala Lys Thr Met Ser Ala Glu Pro Val Ala Val Val
 500 505 510

Glu Leu Pro His Arg Val Pro Tyr Gly Phe His Ala Leu Phe Val Thr
 515 520 525

Glu Glu Gln Leu Gln Glu Gln Thr Leu Ile
 530 535

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 19
 attgaattca tgccttcagc ttcaaac

27

<210> 20
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
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31

<210> 21
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
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38

<210> 22
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
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36

<210> 23
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

cccgggatcc ctcaagcctc tctataccg

29

<210> 24

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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cccgggatcc tttatacgga ttctgaggga g

31

<210> 25

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

attgaattca tggactctgt ttcttcttct tcc

33

<210> 26

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 26

attgaattct taaagcttat taaggtcact ttcc

34

<210> 27

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 27

aagaattcat ggcggagaaa ctcaagtgatg gcagc

35

<210> 28
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 28
 aaaagaattc ggcttatata agagtttggt cctgg 35

<210> 29
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 29
 cgggatccat gcaacactct ctctggtctg atcttcttc 39

<210> 30
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 30
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<210> 31
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 31
 attgaattca tggcttcttt cacggcaacg gc 32

<210> 32
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 32
 gttttcccag tcacgac 17

<210> 33
 <211> 538
 <212> PRT
 <213> Arabidopsis thaliana

<400> 33

Met	Ala	Glu	Lys	Leu	Ser	Asp	Gly	Ser	Ile	Ile	Ile	Ser	Val	His	Pro	1	5	10	15
Arg	Pro	Ser	Lys	Gly	Phe	Ser	Ser	Lys	Leu	Leu	Asp	Leu	Leu	Glu	Arg	20	25	30	
Leu	Val	Val	Lys	Leu	Met	His	Asp	Ala	Ser	Leu	Pro	Leu	His	Tyr	Leu	35	40	45	
Ser	Gly	Asn	Phe	Ala	Pro	Ile	Arg	Asp	Glu	Thr	Pro	Pro	Val	Lys	Asp	50	55	60	
Leu	Pro	Val	His	Gly	Phe	Leu	Pro	Glu	Cys	Leu	Asn	Gly	Glu	Phe	Val	65	70	75	
Arg	Val	Gly	Pro	Asn	Pro	Lys	Phe	Asp	Ala	Val	Ala	Gly	Tyr	His	Trp	85	90	95	
Phe	Asp	Gly	Asp	Gly	Met	Ile	His	Gly	Val	Arg	Ile	Lys	Asp	Gly	Lys	100	105	110	
Ala	Thr	Tyr	Val	Ser	Arg	Tyr	Val	Lys	Thr	Ser	Arg	Leu	Lys	Gln	Glu	115	120	125	
Glu	Phe	Phe	Gly	Ala	Ala	Lys	Phe	Met	Lys	Ile	Gly	Asp	Leu	Lys	Gly	130	135	140	
Phe	Phe	Gly	Leu	Leu	Met	Val	Asn	Val	Gln	Gln	Leu	Arg	Thr	Lys	Leu	145	150	155	
Lys	Ile	Leu	Asp	Asn	Thr	Tyr	Gly	Asn	Gly	Thr	Ala	Asn	Thr	Ala	Leu	165	170	175	
Val	Tyr	His	His	Gly	Lys	Leu	Leu	Ala	Leu	Gln	Glu	Ala	Asp	Lys	Pro	180	185	190	
Tyr	Val	Ile	Lys	Val	Leu	Glu	Asp	Gly	Asp	Leu	Gln	Thr	Leu	Gly	Ile	195	200	205	
Ile	Asp	Tyr	Asp	Lys	Arg	Leu	Thr	His	Ser	Phe	Thr	Ala	His	Pro	Lys	210	215	220	
Val	Asp	Pro	Val	Thr	Gly	Glu	Met	Phe	Thr	Phe	Gly	Tyr	Ser	His	Thr	225	230	235	
Pro	Pro	Tyr	Leu	Thr	Tyr	Arg	Val	Ile	Ser	Lys	Asp	Gly	Ile	Met	His	245	250	255	
Asp	Pro	Val	Pro	Ile	Thr	Ile	Ser	Glu	Pro	Ile	Met	Met	His	Asp	Phe	260	265	270	

Ala Ile Thr Glu Thr Tyr Ala Ile Phe Met Asp Leu Pro Met His Phe
 275 280 285
 Arg Pro Lys Glu Met Val Lys Glu Lys Lys Met Ile Tyr Ser Phe Asp
 290 295 300
 Pro Thr Lys Lys Ala Arg Phe Gly Val Leu Pro Arg Tyr Ala Lys Asp
 305 310 315 320
 Glu Leu Met Ile Arg Trp Phe Glu Leu Pro Asn Cys Phe Ile Phe His
 325 330 335
 Asn Ala Asn Ala Trp Glu Glu Glu Asp Glu Val Val Leu Ile Thr Cys
 340 345 350
 Arg Leu Glu Asn Pro Asp Leu Asp Met Val Ser Gly Lys Val Lys Glu
 355 360 365
 Lys Leu Glu Asn Phe Gly Asn Glu Leu Tyr Glu Met Arg Phe Asn Met
 370 375 380
 Lys Thr Gly Ser Ala Ser Gln Lys Lys Leu Ser Ala Ser Ala Val Asp
 385 390 395 400
 Phe Pro Arg Ile Asn Glu Cys Tyr Thr Gly Lys Lys Gln Arg Tyr Val
 405 410 415
 Tyr Gly Thr Ile Leu Asp Ser Ile Ala Lys Val Thr Gly Ile Ile Lys
 420 425 430
 Phe Asp Leu His Ala Glu Ala Glu Thr Gly Lys Arg Met Leu Glu Val
 435 440 445
 Gly Gly Asn Ile Lys Gly Ile Tyr Asp Leu Gly Glu Gly Arg Tyr Gly
 450 455 460
 Ser Glu Ala Ile Tyr Val Pro Arg Glu Thr Ala Glu Glu Asp Asp Gly
 465 470 475 480
 Tyr Leu Ile Phe Phe Val His Asp Glu Asn Thr Gly Lys Ser Cys Val
 485 490 495
 Thr Val Ile Asp Ala Lys Thr Met Ser Ala Glu Pro Val Ala Val Val
 500 505 510
 Glu Leu Pro His Arg Val Pro Tyr Gly Phe His Ala Leu Phe Val Thr
 515 520 525
 Glu Glu Gln Leu Gln Glu Gln Thr Leu Ile
 530 535